

ctc aac gtg atc aca aca aat cat atc ttg tct aat tgt 401
 Leu Asn Val Ile Thr Thr Asn His Ile Leu Ser Asn Cys
 100 105 110

gag ctg gtt aag aag ttt tta gat cca aac aac tat tcc 440
 Glu Leu Val Lys Lys Phe Leu Asp Pro Asn Asn Tyr Ser
 115 120 125

gca aac tat act gag att gcc ttg caa cag gtt tcc atg 479
 Ala Asn Tyr Thr Glu Ile Ala Leu Gln Gln Val Ser Met
 130 135

ttc ttc cga tca gaa cca aag tgg gag gtg gtg gaa cct 518
 Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu Pro
 140 145 150

ttg aaa gac ata ggt tgg aga ata agg aag aaa tat ttc 557
 Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe
 155 160

ttg atg aag att aaa aat cag cca aag gaa cgg cta gtg 596
 Leu Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val
 165 170 175

tta agc tgg gct gac ctt ggc cca gac aag tat ttg tca 635
 Leu Ser Trp Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser
 180 185 190

gat aaa gat ttt cag tgt cta atc aaa ctt ctg cct tct 674
 Asp Lys Asp Phe Gln Cys Leu Ile Lys Leu Leu Pro Ser
 195 200

tgt ttg cac cct tac atc tat cgg gtt acc ttt gcc aca 713
 Cys Leu His Pro Tyr Ile Tyr Arg Val Thr Phe Ala Thr
 205 210 215

gct aat gaa tcc tca gcg ttg cta att agg atg ttt aac 752
 Ala Asn Glu Ser Ser Ala Leu Leu Ile Arg Met Phe Asn
 220 225

gaa aag gga aca ttg aag gat ctg atc tac aag gca aaa 791
 Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys Ala Lys
 230 235 240

cca aaa gac cca ttt cta aag aag tac tgc aac cct aag 830
 Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys
 245 250 255

aag att cag ggc ctg gaa ctc cag caa ata aaa aca tat 869
 Lys Ile Gln Gly Leu Glu Leu Gln Gln Ile Lys Thr Tyr
 260 265

gga cgg caa ata tta gag gta ctg aag ttt ctt cat gac 908
 Gly Arg Gln Ile Leu Glu Val Leu Lys Phe Leu His Asp
 270 275 280

aag gga ttc cct tat ggg cat ctt cac gcc tcc aat gtg 947
 Lys Gly Phe Pro Tyr Gly His Leu His Ala Ser Asn Val
 285 290

atg ctc gat ggg gac act tgt cgg ctg ctg gac ctt gag 986
 Met Leu Asp Gly Asp Thr Cys Arg Leu Leu Asp Leu Glu
 295 300 305

aat tcc tta ttg ggc ctg cct tcc ttc tac cga tct tat 1025
 Asn Ser Leu Leu Gly Leu Pro Ser Phe Tyr Arg Ser Tyr
 310 315 320

ttt tca caa ttc agg aaa atc aat aca ttg gaa agt gtg 1064
 Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu Glu Ser Val
 325 330

gat gtc cac tgc ttt ggc cac tta ctg tat gaa atg act 1103
 Asp Val His Cys Phe Gly His Leu Leu Tyr Glu Met Thr
 335 340 345

tat gga cga ccg cca gac tcg gtg cct gtg gac tcc ttc 1142
 Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe
 350 355

cct cct gcc ccg tcc atg gct gtg gtg gcc gtg ttg gag 1181
 Pro Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu
 360 365 370

tct acg ctg tct tgt gaa gcc tgt aaa aat ggc atg cct 1220
 Ser Thr Leu Ser Cys Glu Ala Cys Lys Asn Gly Met Pro
 375 380 385

acc atc tcc cgg ctc tta cag atg cca tta ttc agc gat 1259
 Thr Ile Ser Arg Leu Leu Gln Met Pro Leu Phe Ser Asp
 390 395

gtt tta cta acc act tct gaa aaa cca cag ttt aag atc 1298
 Val Leu Leu Thr Thr Ser Glu Lys Pro Gln Phe Lys Ile
 400 405 410

cct aca aag tta aaa gag gca ttg aga att gcc aaa gaa 1337
 Pro Thr Lys Leu Lys Glu Ala Leu Arg Ile Ala Lys Glu
 415 420

tgt ata gag aag aga cta att gag gaa cag aaa cag att 1376
 Cys Ile Glu Lys Arg Leu Ile Glu Glu Gln Lys Gln Ile
 425 430 435

cac cag cat cga aga ctg aca aga gct cag tcc cac cat 1415
 His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His
 440 445 450

gga tct gag gag gaa aga aaa aaa aga aag att tta gct 1454
 Gly Ser Glu Glu Glu Arg Lys Lys Arg Lys Ile Leu Ala
 455 460

cga aag aag tca aaa cga tct gct ctt gaa aat agt gaa 1493
 Arg Lys Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu
 465 470 475

gag cat tca gcg agg tac agc aac tcc aat aat tca gga 1532
 Glu His Ser Ala Arg Tyr Ser Asn Ser Asn Asn Ser Gly
 480 485

tct ggg gcc agc tca cct ctc acg tcc ccg tca tcg cca 1571

Ser Gly Ala Ser Ser Pro Leu Thr Ser Pro Ser Ser Pro
 490 495 500
 act cca ccc tct aca tca ggg ata tct gca tta cct cca 1610
 Thr Pro Pro Ser Thr Ser Gly Ile Ser Ala Leu Pro Pro
 505 510 515
 cct cct cca cct cca cca cca cca gca gct ccc ttg cct 1649
 Pro Pro Pro Pro Pro Pro Pro Pro Pro Ala Ala Pro Leu Pro
 520 525
 cct gcg agc acc gag gta cct gcc cag ctc tcg tct cag 1688
 Pro Ala Ser Thr Glu Val Pro Ala Gln Leu Ser Ser Gln
 530 535 540
 gct gtg aat ggc atg agc cga ggg gcc ttg ctc agc tcc 1727
 Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser
 545 550
 atc cag aat ttc caa aaa gga act ttg agg aaa gcc aaa 1766
 Ile Gln Asn Phe Gln Lys Gly Thr Leu Arg Lys Ala Lys
 555 560 565
 acc tgt gat cac agt gct ccg aag atc ggc tg aa 1800
 Thr Cys Asp His Ser Ala Pro Lys Ile Gly
 570 575 577
 gcttctgtgt tacacttgga gggaaaagtt cttttttatt cctactcacc 1850
 cctaccccc aaactaccct cttcctggga aagtaattgc tgagccagta 1900
 cagccacaaa cagtactatt ttgcagatgc tcatgtaagc agcttttcga 1950
 gagaaataat tctttaagca gaataaagtt aggctggcat tgctccctta 2000
 agatcttgct cctttattaa ccctgtaaag gagtcttggt tctcctctaa 2050
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 ggaaatagac agaaaaacaa tgacaatatt caatcacagc agtaaattggc 2150
 ctttgtgttg caatcccttc taccatca gacagctcct agaaacattc 2200
 cttacagttc atttctctaa agcattttct gattcttaga taactccaat 2250
 ttttgctacc tttatcttag acattaacac tatagcccaa agcatagtta 2300
 ctttgctaaa tcagaaagca actgagttct ttgttttctc ctcaaataga 2350
 atggggaacg ttcacaacat tctcttaagt tctaacagga ataccattgt 2400
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 ttttagttag atgtattgaa acagacaaaa atattaacat cagaaaaagc 2500
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 tgaggggggc aggtcattgt tacaacagaa gtaaatttgg catctataga 2600
 aatcaattat gatttttgaa agatttatct aaatatatca atatagcatc 2650

tctttaatgt tagtcattta ttagaaagat cctttatcct gatttgctta 2700
aacctttcaa taaattgcac tttaaaggat tataaataat ccatttaaaa 2750
attcaagtac acacatcagt gttggttact atgcagagaa tgtcattgtg 2800
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gtcaagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2891

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<212> PRT
<213> Homo sapiens

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Asp Thr Val Pro Leu Thr Ala Ala Ile Glu Ala Ser Gln Ser Leu
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Gln Ser His Thr Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser
35 40 45
Val Glu Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp
50 55 60
Leu Leu Asn Asn Ser Leu Gln Ile Ala Gly Leu Ser Leu Pro Leu
65 70 75
Pro Pro Lys Lys Leu Ile Gly Asn Met Asp Arg Glu Phe Ile Ala
80 85 90
Glu Arg Gln Lys Gly Leu Gln Asn Tyr Leu Asn Val Ile Thr Thr
95 100 105
Asn His Ile Leu Ser Asn Cys Glu Leu Val Lys Lys Phe Leu Asp
110 115 120
Pro Asn Asn Tyr Ser Ala Asn Tyr Thr Glu Ile Ala Leu Gln Gln
125 130 135
Val Ser Met Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu
140 145 150
Pro Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe Leu
155 160 165
Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val Leu Ser Trp
170 175 180
Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser Asp Lys Asp Phe Gln
185 190 195
Cys Leu Ile Lys Leu Leu Pro Ser Cys Leu His Pro Tyr Ile Tyr
200 205 210
Arg Val Thr Phe Ala Thr Ala Asn Glu Ser Ser Ala Leu Leu Ile
215 220 225

Arg	Met	Phe	Asn	Glu	Lys	Gly	Thr	Leu	Lys	Asp	Leu	Ile	Tyr	Lys	230	235	240
Ala	Lys	Pro	Lys	Asp	Pro	Phe	Leu	Lys	Lys	Tyr	Cys	Asn	Pro	Lys	245	250	255
Lys	Ile	Gln	Gly	Leu	Glu	Leu	Gln	Gln	Ile	Lys	Thr	Tyr	Gly	Arg	260	265	270
Gln	Ile	Leu	Glu	Val	Leu	Lys	Phe	Leu	His	Asp	Lys	Gly	Phe	Pro	275	280	285
Tyr	Gly	His	Leu	His	Ala	Ser	Asn	Val	Met	Leu	Asp	Gly	Asp	Thr	290	295	300
Cys	Arg	Leu	Leu	Asp	Leu	Glu	Asn	Ser	Leu	Leu	Gly	Leu	Pro	Ser	305	310	315
Phe	Tyr	Arg	Ser	Tyr	Phe	Ser	Gln	Phe	Arg	Lys	Ile	Asn	Thr	Leu	320	325	330
Glu	Ser	Val	Asp	Val	His	Cys	Phe	Gly	His	Leu	Leu	Tyr	Glu	Met	335	340	345
Thr	Tyr	Gly	Arg	Pro	Pro	Asp	Ser	Val	Pro	Val	Asp	Ser	Phe	Pro	350	355	360
Pro	Ala	Pro	Ser	Met	Ala	Val	Val	Ala	Val	Leu	Glu	Ser	Thr	Leu	365	370	375
Ser	Cys	Glu	Ala	Cys	Lys	Asn	Gly	Met	Pro	Thr	Ile	Ser	Arg	Leu	380	385	390
Leu	Gln	Met	Pro	Leu	Phe	Ser	Asp	Val	Leu	Leu	Thr	Thr	Ser	Glu	395	400	405
Lys	Pro	Gln	Phe	Lys	Ile	Pro	Thr	Lys	Leu	Lys	Glu	Ala	Leu	Arg	410	415	420
Ile	Ala	Lys	Glu	Cys	Ile	Glu	Lys	Arg	Leu	Ile	Glu	Glu	Gln	Lys	425	430	435
Gln	Ile	His	Gln	His	Arg	Arg	Leu	Thr	Arg	Ala	Gln	Ser	His	His	440	445	450
Gly	Ser	Glu	Glu	Glu	Arg	Lys	Lys	Arg	Lys	Ile	Leu	Ala	Arg	Lys	455	460	465
Lys	Ser	Lys	Arg	Ser	Ala	Leu	Glu	Asn	Ser	Glu	Glu	His	Ser	Ala	470	475	480
Arg	Tyr	Ser	Asn	Ser	Asn	Asn	Ser	Gly	Ser	Gly	Ala	Ser	Ser	Pro	485	490	495
Leu	Thr	Ser	Pro	Ser	Ser	Pro	Thr	Pro	Pro	Ser	Thr	Ser	Gly	Ile	500	505	510
Ser	Ala	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Ala	515	520	525
Pro	Leu	Pro	Pro	Ala	Ser	Thr	Glu	Val	Pro	Ala	Gln	Leu	Ser	Ser			

530	535	540
Gln Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser Ile		
545	550	555
Gln Asn Phe Gln Lys Gly Thr Leu Arg Lys Ala Lys Thr Cys Asp		
560	565	570
His Ser Ala Pro Lys Ile Gly		
575		

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 gtgaacatag atacagctct ttcccccttc cccccctttt aaatgtaaca 150
 aatacttttt atgttcccc tcccccttc cccttttccc ctttccccctt 200
 ttggaaacgt gtcaggaacc aaatagttta agatgagcag ttgaggggac 250
 tgagagagtg atcgacacag aacctggctt cttcgtgctt catcataagt 300
 cgtgctgccg gccaggttac ttaagcacc ttttaacaag gaaaccttgt 350
 gggagatcca gctggccgac tcgagttcag aaacaggacc acagagggtta 400
 cactctggga tcctggccat gaggttggat gcctcacctt actgaaagga 450
 gacactggac ctaa atg gcg cag cat gat ttt gtt cct gct 491
 Met Ala Gln His Asp Phe Val Pro Ala
 1 5
 tgg cta aat ttc tca aca cca cag tca gct aag tca cct 530
 Trp Leu Asn Phe Ser Thr Pro Gln Ser Ala Lys Ser Pro
 10 15 20
 act gcc acc ttc gaa aaa cac gga gag cac cta ccc aga 569
 Thr Ala Thr Phe Glu Lys His Gly Glu His Leu Pro Arg
 25 30 35
 gga gaa ggt aga ttt gga gta agc cgc cgt cga cat aat 608
 Gly Glu Gly Arg Phe Gly Val Ser Arg Arg Arg His Asn
 40 45
 tcc tct gat ggt ttt ttt aac aat ggt ccc cta cga act 647
 Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg Thr
 50 55 60
 gca gga gat tct tgg cac cag ccc tcc tgt tcc gcc atg 686
 Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met
 65 70
 att ctg tgg act ctg gtg tct cta agg gag cat atg ctg 725
 Ile Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu

75		80		85	
gaa tca cag gga acc cat ctg gtt ggc ata gct ctt ccc 764					
Glu Ser Gln Gly Thr His Leu Val Gly Ile Ala Leu Pro					
90		95		100	
cga ggt cat gat ggc atg agc caa cgt agt gta ggt ggc 803					
Arg Gly His Asp Gly Met Ser Gln Arg Ser Val Gly Gly					
105		110			
aca ggg aac cat cgc cat tgg aat ggc agc ttc cac tcc 842					
Thr Gly Asn His Arg His Trp Asn Gly Ser Phe His Ser					
115		120		125	
cgg aaa ggg tgt gct ttt cag gaa aag cca cct atg gag 881					
Arg Lys Gly Cys Ala Phe Gln Glu Lys Pro Pro Met Glu					
130		135			
att agg gaa gaa aag aaa gaa gac aag gtg gaa aag ttg 920					
Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu Lys Leu					
140		145		150	
cag ttt gaa gag gag gac ttt cct tcc ttg aat cca gaa 959					
Gln Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu					
155		160		165	
gct ggc aaa cag cat cag cca tgc aga cct att ggg aca 998					
Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr					
170		175			
cct tct gga gta tgg gaa aac ccg cct agt gcc aag caa 1037					
Pro Ser Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln					
180		185		190	
ccc tcc aag atg cta gtt atc aaa aaa gtt tcc aaa gag 1076					
Pro Ser Lys Met Leu Val Ile Lys Lys Val Ser Lys Glu					
195		200			
gat cct gct gct gcc ttc tct gct gca ttc acc tca cca 1115					
Asp Pro Ala Ala Ala Phe Ser Ala Ala Phe Thr Ser Pro					
205		210		215	
gga tct cac cat gca aat ggg aac aaa ttg tca tcc gtg 1154					
Gly Ser His His Ala Asn Gly Asn Lys Leu Ser Ser Val					
220		225		230	
gtt cca agt gtc tat aag aac ctg gtt cct aag cct gta 1193					
Val Pro Ser Val Tyr Lys Asn Leu Val Pro Lys Pro Val					
235		240			
cca cct cct tcc aag cct aat gca tgg aaa gct aac agg 1232					
Pro Pro Pro Ser Lys Pro Asn Ala Trp Lys Ala Asn Arg					
245		250		255	
atg gag cac aag tca gga tcc ctt tcc tct agc cgg gag 1271					
Met Glu His Lys Ser Gly Ser Leu Ser Ser Ser Arg Glu					
260		265			
tct gct ttt acc agt cca atc tcc gtt acc aaa cca gtg 1310					
Ser Ala Phe Thr Ser Pro Ile Ser Val Thr Lys Pro Val					
270		275		280	

gta ctg gct agt ggt gca gct ctg agt tct ccc aaa gag 1349
 Val Leu Ala Ser Gly Ala Ala Leu Ser Ser Pro Lys Glu
 285 290 295

agt ccc tcc agc acc acc cct cca att gag atc agc tcc 1388
 Ser Pro Ser Ser Thr Thr Pro Pro Ile Glu Ile Ser Ser
 300 305

tct cgt ctg acc aag ttg acc cgc cga acc acc gac agg 1427
 Ser Arg Leu Thr Lys Leu Thr Arg Arg Thr Thr Asp Arg
 310 315 320

aag agt gag ttc ctg aaa act ctg aag gat gac cgg aat 1466
 Lys Ser Glu Phe Leu Lys Thr Leu Lys Asp Asp Arg Asn
 325 330

gga gac ttc tca gag aat aga gac tgt gac aag ctg gaa 1505
 Gly Asp Phe Ser Glu Asn Arg Asp Cys Asp Lys Leu Glu
 335 340 345

gat ttg gag gac aac agc aca cct gaa cca aag gaa aat 1544
 Asp Leu Glu Asp Asn Ser Thr Pro Glu Pro Lys Glu Asn
 350 355 360

ggg gag gaa ggc tgt cat caa aat ggt ctt gcc ctc cct 1583
 Gly Glu Glu Gly Cys His Gln Asn Gly Leu Ala Leu Pro
 365 370

gta gtg gaa gaa ggg gag gtt ctc tca cac tct cta gaa 1622
 Val Val Glu Glu Gly Glu Val Leu Ser His Ser Leu Glu
 375 380 385

gca gag cac agg tta ttg aaa gct atg ggt tgg cag gaa 1661
 Ala Glu His Arg Leu Leu Lys Ala Met Gly Trp Gln Glu
 390 395

tat cct gaa aat gat gag aat tgc ctt ccc ctc aca gag 1700
 Tyr Pro Glu Asn Asp Glu Asn Cys Leu Pro Leu Thr Glu
 400 405 410

gat gag ctc aaa gag ttc cac atg aag aca gag cag ctg 1739
 Asp Glu Leu Lys Glu Phe His Met Lys Thr Glu Gln Leu
 415 420 425

aga aga aat ggc ttt gga aag aat ggc ttc ttg cag agc 1778
 Arg Arg Asn Gly Phe Gly Lys Asn Gly Phe Leu Gln Ser
 430 435

cgc agt tcc agt ctg ttc tcc cct tgg aga agc act tgc 1817
 Arg Ser Ser Ser Leu Phe Ser Pro Trp Arg Ser Thr Cys
 440 445 450

aaa gca gag ttt gag gac tca gac acc gaa acc agt agc 1856
 Lys Ala Glu Phe Glu Asp Ser Asp Thr Glu Thr Ser Ser
 455 460

agt gaa aca tca gat gac gat gcc tgg aag t agg 1890
 Ser Glu Thr Ser Asp Asp Asp Ala Trp Lys
 465 470 474

catataaatg ctcacagtta aatctgaccc agtaaactct gtgtgttttag 1940
 ggagtataca aaagaaatcg ttcttttctt tttcttatgt tgttgaatac 1990
 ttcattcaca agggaaataa tcatatccca aagagagaaa aaaaaaaaaa 2040
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 <211> 474
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 Glu His Leu Pro Arg Gly Glu Gly Arg Phe Gly Val Ser Arg Arg
 35 40 45
 Arg His Asn Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg
 50 55 60
 Thr Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met Ile
 65 70 75
 Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu Glu Ser Gln
 80 85 90
 Gly Thr His Leu Val Gly Ile Ala Leu Pro Arg Gly His Asp Gly
 95 100 105
 Met Ser Gln Arg Ser Val Gly Gly Thr Gly Asn His Arg His Trp
 110 115 120
 Asn Gly Ser Phe His Ser Arg Lys Gly Cys Ala Phe Gln Glu Lys
 125 130 135
 Pro Pro Met Glu Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu
 140 145 150
 Lys Leu Gln Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu
 155 160 165
 Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr Pro Ser
 170 175 180
 Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln Pro Ser Lys Met
 185 190 195
 Leu Val Ile Lys Lys Val Ser Lys Glu Asp Pro Ala Ala Ala Phe
 200 205 210
 Ser Ala Ala Phe Thr Ser Pro Gly Ser His His Ala Asn Gly Asn
 215 220 225

Lys	Leu	Ser	Ser	Val	Val	Pro	Ser	Val	Tyr	Lys	Asn	Leu	Val	Pro	230	235	240
Lys	Pro	Val	Pro	Pro	Pro	Ser	Lys	Pro	Asn	Ala	Trp	Lys	Ala	Asn	245	250	255
Arg	Met	Glu	His	Lys	Ser	Gly	Ser	Leu	Ser	Ser	Ser	Arg	Glu	Ser	260	265	270
Ala	Phe	Thr	Ser	Pro	Ile	Ser	Val	Thr	Lys	Pro	Val	Val	Leu	Ala	275	280	285
Ser	Gly	Ala	Ala	Leu	Ser	Ser	Pro	Lys	Glu	Ser	Pro	Ser	Ser	Thr	290	295	300
Thr	Pro	Pro	Ile	Glu	Ile	Ser	Ser	Ser	Arg	Leu	Thr	Lys	Leu	Thr	305	310	315
Arg	Arg	Thr	Thr	Asp	Arg	Lys	Ser	Glu	Phe	Leu	Lys	Thr	Leu	Lys	320	325	330
Asp	Asp	Arg	Asn	Gly	Asp	Phe	Ser	Glu	Asn	Arg	Asp	Cys	Asp	Lys	335	340	345
Leu	Glu	Asp	Leu	Glu	Asp	Asn	Ser	Thr	Pro	Glu	Pro	Lys	Glu	Asn	350	355	360
Gly	Glu	Glu	Gly	Cys	His	Gln	Asn	Gly	Leu	Ala	Leu	Pro	Val	Val	365	370	375
Glu	Glu	Gly	Glu	Val	Leu	Ser	His	Ser	Leu	Glu	Ala	Glu	His	Arg	380	385	390
Leu	Leu	Lys	Ala	Met	Gly	Trp	Gln	Glu	Tyr	Pro	Glu	Asn	Asp	Glu	395	400	405
Asn	Cys	Leu	Pro	Leu	Thr	Glu	Asp	Glu	Leu	Lys	Glu	Phe	His	Met	410	415	420
Lys	Thr	Glu	Gln	Leu	Arg	Arg	Asn	Gly	Phe	Gly	Lys	Asn	Gly	Phe	425	430	435
Leu	Gln	Ser	Arg	Ser	Ser	Ser	Leu	Phe	Ser	Pro	Trp	Arg	Ser	Thr	440	445	450
Cys	Lys	Ala	Glu	Phe	Glu	Asp	Ser	Asp	Thr	Glu	Thr	Ser	Ser	Ser	455	460	465
Glu	Thr	Ser	Asp	Asp	Asp	Ala	Trp	Lys							470		

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<211> 294

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

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 cgacacggtg ccgctgacag cagccatcga ggcgagccag agcctgcagt 100
 cccacacgga atatattatt cgagtgcaaa gaggaatttc tctggaaaac 150
 agctggcaga tngtnagaag atacagtgcac ttnnatntgc ttaacaacag 200
 cttncanatt ncaggncctna gnntncctct tcctccnaan aaantgattn 250
 ggnaacatgg ancgtnant tcatngctng anaggcagnn aggt 294

<210> 6
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 <212> DNA
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<400> 6
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<210> 7
 <211> 51
 <212> DNA
 <213> Homo sapiens

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 a 51

<210> 8
 <211> 31
 <212> DNA
 <213> Homo sapiens

<400> 8
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<210> 9
 <211> 793
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 379, 433, 459, 492, 517, 541, 549, 561, 575, 579, 582, 710, 742,
 774, 784
 <223> unknown base

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 ggactttcct tccttgaatc cagaagctgg caaacagcat cagccatgca 100
 gacctattgg gacaccttct ggagtatggg aaaacccgcc tagtgccaag 150
 caaccctcca agatgctagt tatcaaaaaa gtttccaaag aggatcctgc 200
 tgctgcyytc tctgctgcat tcacctcacc aggatctcac catgcaaata 250

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 gaagragtga ngttcctgaa aactnctgna anggatgacc gggaatggga 600
 agacttityc agaagaatag agactgtgac aagctggaag atttgaggga 650
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cag gga gtg gtn cta aca gcc tac cac ccc agc ggc aag	130											
Gln Gly Val Xaa Leu Thr Ala Tyr His Pro Ser Gly Lys												
10 15 20												
gac cag acc gtc ggg aac agc cat gca aag gca ggg gag	169											
Asp Gln Thr Val Gly Asn Ser His Ala Lys Ala Gly Glu												
25 30												
gaa gcc acc tcg agt cgc aga tat ggc cag tac act atg	208											
Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr Met												
35 40 45												
aac cag gaa agc acc acc atc aaa gtt atg gag aag cct	247											
Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro												
50 55												
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Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu												
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Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile												
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Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val												
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Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu Glu Glu												
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Glu Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly												
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Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile Val Phe Leu												
125 130 135												
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Ser Thr Leu Thr Arg Thr Gln Ala Ala Ala Val Gln Lys												
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Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn												
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Lys Gln Tyr Gln Ile Pro Asp Val Arg Asp Ile Phe Ala												
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Gln Gln Arg Glu Ser Lys Glu Thr Ala Pro Gly Gly Thr												
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gaa tcg cag tca ctt aga aca aat gaa aac aaa tac caa	676											
Glu Ser Gln Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln												

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Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu Glu					
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aag ctg atc cca cct gag gag acg cct gcc cct gaa aca 754					
Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr					
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gac atc aac ctg gag gta tca ttt gcc gag caa gca ctc 793					
Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu					
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Asn Gln Lys Glu Arg Ser Lys Glu Lys Ile Gln Lys Ser					
245		250			
aaa ggc gat gat gcc aca tta cct agt ttc aga ttg cca 871					
Lys Gly Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro					
255		260		265	
aaa gac aaa acg ggt acc aca agg att ggt gac ctc gca 910					
Lys Asp Lys Thr Gly Thr Thr Arg Ile Gly Asp Leu Ala					
270		275		280	
ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att 949					
Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile					
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Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu					
295		300		305	
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Lys Gln Gln Lys Ala Val Lys Ile Lys Thr Lys Asp Ser					
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Gly Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln					
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Asp Gln Arg Lys Val Pro Gly Met Arg Ile Pro Leu Ile					
335		340		345	
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Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu					
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Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile					
360		365		370	
aga atc aag aat ctt tgc caa gaa cta gaa gca aag ttt 1222					
Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe					
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tat gaa ggg act ttt aat tgg gaa agt gtc aaa cag cat 1261					
Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His					
385		390		395	

gat gcc gcc agc ctg ctg aag ctc ttc att cgg gag ttg 1300
Asp Ala Ala Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu
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ccc cag cca ctg ctc agt gtg gag tat ctc aaa gcc ttt 1339
Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu Lys Ala Phe
415 420

cag gct gtc cag aat ctt cca acc aag aag cag caa cta 1378
Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu
425 430 435

cag gct ttg aac ctt ctt gtc atc ctc cta cct gat gca 1417
Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp Ala
440 445

aac agg gac aca ctg aag gcc ctt ctt gaa ttt ctc caa 1456
Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln
450 455 460

aga gta ata gat aat aaa gaa aaa aat aaa atg aca gtc 1495
Arg Val Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val
465 470 475

atg aat gta gca atg gtc atg gcc ccg aat ctc ttt atg 1534
Met Asn Val Ala Met Val Met Ala Pro Asn Leu Phe Met
480 485

tgt cat gca ttg gga ttg aag tcc agt gaa cag cga gaa 1573
Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu
490 495 500

ttt gta atg gca gct ggg aca gca aat acc atg cac tta 1612
Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met His Leu
505 510

ttg att aag tac caa aaa ctt ctg tgg aca att ccc aag 1651
Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys
515 520 525

ttt att gta aac caa gtg agg aag caa aac acg gaa aat 1690
Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn
530 535 540

cat aaa aag gat aaa aga gcc atg aag aaa ttg ctg aag 1729
His Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys
545 550

aaa atg gct tat gac cga gaa aaa tat gaa aag caa gat 1768
Lys Met Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp
555 560 565

aag agt aca aat gat gct gac gtt cct cag gga gtg att 1807
Lys Ser Thr Asn Asp Ala Asp Val Pro Gln Gly Val Ile
570 575

cga gtg caa gct ccc cat ctt tcg aaa gtt tcc atg gca 1846
Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala
580 585 590

ata cag cta act gaa gaa cta aaa gcc agt gat gta ctt 1885
 Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu
 595 600 605

gcc agg ttt ctc agc caa gaa agt ggg gtt gcc cag act 1924
 Ala Arg Phe Leu Ser Gln Glu Ser Gly Val Ala Gln Thr
 610 615

ctc aag aaa gga gaa gtt ttt ttg tat gaa att gga gga 1963
 Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly Gly
 620 625 630

aat att ggg gaa cgc tgc ctt gat gat gac act tac atg 2002
 Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met
 635 640

aag gat tta tat cag ctt aac cca aat gct gag tgg gtt 2041
 Lys Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val
 645 650 655

ata aag tca aag cca ttg t agaagactta acaagctgca 2080
 Ile Lys Ser Lys Pro Leu
 660 663

gataaccatg tggacttctg tcataattct tgctgagtca agagtgtaaa 2130
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 aaatgactct cttaagcctt aaaaagtcac agatttgtgc tgctgccaga 2230
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<212> PRT

<213> Homo sapiens

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Ala Gly Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr
 35 40 45

Met Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro
 50 55 60

Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met
 65 70 75

Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu
 80 85 90

Asn Ser Gln Glu Asp Gln Glu Val Val Val Val Lys Glu Pro Asp

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Phe	Leu	Ser	Thr	Leu	Thr	Arg	Thr	Gln	Ala	Ala	Ala	Val	Gln	Lys					
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Arg	Val	Glu	Thr	Val	Ser	Gln	Thr	Leu	Arg	Lys	Lys	Asn	Lys	Gln					
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Tyr	Gln	Ile	Pro	Asp	Val	Arg	Asp	Ile	Phe	Ala	Gln	Gln	Arg	Glu					
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Ser	Lys	Glu	Thr	Ala	Pro	Gly	Gly	Thr	Glu	Ser	Gln	Ser	Leu	Arg					
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Thr	Asn	Glu	Asn	Lys	Tyr	Gln	Gly	Arg	Asp	Asp	Glu	Ala	Ser	Asn					
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Leu	Val	Gly	Glu	Glu	Lys	Leu	Ile	Pro	Pro	Glu	Glu	Thr	Pro	Ala					
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Pro	Glu	Thr	Asp	Ile	Asn	Leu	Glu	Val	Ser	Phe	Ala	Glu	Gln	Ala					
				230					235					240					
Leu	Asn	Gln	Lys	Glu	Arg	Ser	Lys	Glu	Lys	Ile	Gln	Lys	Ser	Lys					
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Gly	Asp	Asp	Ala	Thr	Leu	Pro	Ser	Phe	Arg	Leu	Pro	Lys	Asp	Lys					
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Thr	Gly	Thr	Thr	Arg	Ile	Gly	Asp	Leu	Ala	Pro	Gln	Asp	Met	Lys					
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Lys	Val	Cys	His	Leu	Ala	Leu	Ile	Glu	Leu	Thr	Ala	Leu	Tyr	Asp					
				290					295					300					
Val	Leu	Gly	Ile	Glu	Leu	Lys	Gln	Gln	Lys	Ala	Val	Lys	Ile	Lys					
				305					310					315					
Thr	Lys	Asp	Ser	Gly	Leu	Phe	Cys	Val	Pro	Leu	Thr	Ala	Leu	Leu					
				320					325					330					
Glu	Gln	Asp	Gln	Arg	Lys	Val	Pro	Gly	Met	Arg	Ile	Pro	Leu	Ile					
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Phe	Gln	Lys	Leu	Ile	Ser	Arg	Ile	Glu	Glu	Arg	Gly	Leu	Glu	Thr					
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Glu	Gly	Leu	Leu	Arg	Ile	Pro	Gly	Ala	Ala	Ile	Arg	Ile	Lys	Asn					
				365					370					375					
Leu	Cys	Gln	Glu	Leu	Glu	Ala	Lys	Phe	Tyr	Glu	Gly	Thr	Phe	Asn					
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Trp	Glu	Ser	Val	Lys	Gln	His	Asp	Ala	Ala	Ser	Leu	Leu	Lys	Leu					
				395					400					405					

Phe Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu	410	415	420
Lys Ala Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln	425	430	435
Leu Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp Ala Asn	440	445	450
Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln Arg Val Ile	455	460	465
Asp Asn Lys Glu Lys Asn Lys Met Thr Val Met Asn Val Ala Met	470	475	480
Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly Leu Lys	485	490	495
Ser Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn	500	505	510
Thr Met His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile	515	520	525
Pro Lys Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn	530	535	540
His Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met	545	550	555
Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn	560	565	570
Asp Ala Asp Val Pro Gln Gly Val Ile Arg Val Gln Ala Pro His	575	580	585
Leu Ser Lys Val Ser Met Ala Ile Gln Leu Thr Glu Glu Leu Lys	590	595	600
Ala Ser Asp Val Leu Ala Arg Phe Leu Ser Gln Glu Ser Gly Val	605	610	615
Ala Gln Thr Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly	620	625	630
Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met Lys	635	640	645
Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val Ile Lys Ser	650	655	660

Lys Pro Leu

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<211> 1327

<212> DNA

<213> Homo sapiens

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 <222> 74, 1306
 <223> unknown base

<400> 15

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gtggggcagg ggtgtggctg ccccgcccg cagcctgca cctgtctcct 200

ctttgtgacc agtaccgcaa ggggatcatc tcgggctccg tctgccagga 250

cctgtgtgag ctgcat      atg gtg gag tgg agg acc tgc ctc 290
                        Met Val Glu Trp Arg Thr Cys Leu
                          1          5

tcg gtg gcc ccg ggc cag cag gtg tac agc ggg ctc tgg 329
Ser Val Ala Pro Gly Gln Gln Val Tyr Ser Gly Leu Trp
      10          15          20

cgg gac aag gat gta acc atc aag tgt ggc att gag gag 368
Arg Asp Lys Asp Val Thr Ile Lys Cys Gly Ile Glu Glu
              25          30

acc ctc gac tcc aag gcc cgg tcg gat gcg gcc ccc cgg 407
Thr Leu Asp Ser Lys Ala Arg Ser Asp Ala Ala Pro Arg
      35          40          45

cgg gag ctg gta ctg ttt gac aag ccc acc cgg ggc acc 446
Arg Glu Leu Val Leu Phe Asp Lys Pro Thr Arg Gly Thr
      50          55          60

tcc atc aag gaa ttc cgg gag atg acc ctc ggc ttc ctc 485
Ser Ile Lys Glu Phe Arg Glu Met Thr Leu Gly Phe Leu
              65          70

aag gcg aac ctg gga gac ctg cct tcc ctg ccg gcg ctg 524
Lys Ala Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala Leu
      75          80          85

gtt ggc cag gtc ctg ctc atg gct gac ttc aac aag gac 563
Val Gly Gln Val Leu Leu Met Ala Asp Phe Asn Lys Asp
      90          95

aac cgg gtg tcc ctg gcg gaa gcc aag tcc gtg tgg gcc 602
Asn Arg Val Ser Leu Ala Glu Ala Lys Ser Val Trp Ala
     100          105          110

ctg ctg cag cgt aac gag ttc ctg ctg ctg ctg tcc ctg 641
Leu Leu Gln Arg Asn Glu Phe Leu Leu Leu Leu Ser Leu
     115          120          125

cag gag aag gag cac gcc tcc aga ctg ctg ggc tac tgt 680
Gln Glu Lys Glu His Ala Ser Arg Leu Leu Gly Tyr Cys
     130          135

ggg gac ctc tac ctc acc gag ggc gtg ccg cat ggc gcc 719
Gly Asp Leu Tyr Leu Thr Glu Gly Val Pro His Gly Ala

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Trp His Ala Ala Ala Leu Pro Pro Leu Leu Arg Pro Leu			
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Leu Pro Pro Ala Leu Gln Gly Ala Leu Gln Gln Trp Leu			
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ggg cct gcg tgg cct tgg cgg gcc aag atc gcc atc ggc 836			
Gly Pro Ala Trp Pro Trp Arg Ala Lys Ile Ala Ile Gly			
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ctg ctg gag ttc gtg gag gag ctc ttc cac ggc tct tac 875			
Leu Leu Glu Phe Val Glu Glu Leu Phe His Gly Ser Tyr			
195	200		
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Gly Thr Phe Tyr Met Cys Glu Thr Thr Leu Ala Asn Val			
205	210	215	
ggc tac aca gcc acc tac gac ttc aag atg gcc gac ctg 953			
Gly Tyr Thr Ala Thr Tyr Asp Phe Lys Met Ala Asp Leu			
220	225		
cag cag gtg gca ccc gag gcc acc gtg cgc cgc ttc ctg 992			
Gln Gln Val Ala Pro Glu Ala Thr Val Arg Arg Phe Leu			
230	235	240	
cag ggc cgc cgc tgc gag cac agc acc gac tgc acc tac 1031			
Gln Gly Arg Arg Cys Glu His Ser Thr Asp Cys Thr Tyr			
245	250	255	
ggg cgc gac tgc agg gcc ccg tgt gac agg ctc atg agg 1070			
Gly Arg Asp Cys Arg Ala Pro Cys Asp Arg Leu Met Arg			
260	265		
cag tgc aag ggc gac ctc atc cag ccc aac ctg gcc aag 1109			
Gln Cys Lys Gly Asp Leu Ile Gln Pro Asn Leu Ala Lys			
270	275	280	
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285	290		
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295	300	305	
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Thr Cys Thr Thr Leu Ser Gly Leu Ala Ser Gln Val Glu			
310	315	320	
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325	330		
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<211> 344

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 104

<223> unknown amino acid

<400> 16

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Gly	Ile	Glu	Glu	Thr	Leu	Asp	Ser	Lys	Ala	Arg	Ser	Asp	Ala	Ala	
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Pro	Arg	Arg	Glu	Leu	Val	Leu	Phe	Asp	Lys	Pro	Thr	Arg	Gly	Thr	
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Ser	Ile	Lys	Glu	Phe	Arg	Glu	Met	Thr	Leu	Gly	Phe	Leu	Lys	Ala	
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Asn	Leu	Gly	Asp	Leu	Pro	Ser	Leu	Pro	Ala	Leu	Val	Gly	Gln	Val	
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Glu	Ala	Lys	Ser	Val	Trp	Ala	Leu	Leu	Gln	Arg	Asn	Glu	Phe	Leu	
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Ala	Trp	His	Ala	Ala	Ala	Leu	Pro	Pro	Leu	Leu	Arg	Pro	Leu	Leu	
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Pro	Pro	Ala	Leu	Gln	Gly	Ala	Leu	Gln	Gln	Trp	Leu	Gly	Pro	Ala	
				170					175					180	
Trp	Pro	Trp	Arg	Ala	Lys	Ile	Ala	Ile	Gly	Leu	Leu	Glu	Phe	Val	
				185					190					195	
Glu	Glu	Leu	Phe	His	Gly	Ser	Tyr	Gly	Thr	Phe	Tyr	Met	Cys	Glu	
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				215					220					225	
Met	Ala	Asp	Leu	Gln	Gln	Val	Ala	Pro	Glu	Ala	Thr	Val	Arg	Arg	
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Phe	Leu	Gln	Gly	Arg	Arg	Cys	Glu	His	Ser	Thr	Asp	Cys	Thr	Tyr
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Gly	Arg	Asp	Cys	Arg	Ala	Pro	Cys	Asp	Arg	Leu	Met	Arg	Gln	Cys
				260					265					270
Lys	Gly	Asp	Leu	Ile	Gln	Pro	Asn	Leu	Ala	Lys	Val	Cys	Ala	Leu
				275					280					285
Leu	Arg	Gly	Tyr	Leu	Leu	Pro	Gly	Ala	Pro	Ala	Asp	Leu	Arg	Glu
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Glu	Leu	Gly	Thr	Gln	Leu	Arg	Thr	Cys	Thr	Thr	Leu	Ser	Gly	Leu
				305					310					315
Ala	Ser	Gln	Val	Glu	Ala	His	His	Ser	Leu	Val	Leu	Ser	His	Leu
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Lys	Thr	Leu	Leu	Trp	Lys	Lys	Ile	Ser	Asn	Thr	Lys	Tyr	Ser	
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 1924, 1939, 1953, 1982, 1991-1992, 2000, 2443
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 tgctctngng cncggcaant cnggggagct actgcaccag gggcgctacc 150
 gggagccctg gcgcgcctg cgaggncctgc gaggcagaacc cagtgacttg 200
 attgtaaaaa ttacagagc ggaatcatat gctgggtctcc aagagtttaa 250
 agcagcctta gaagatttaa atg cag ttc ttt ttc aac ttc 291
 Met Gln Phe Phe Phe Asn Phe
 1 5

 caa gat tgg cct gaa ggt cta ctt cag gaa ang gaa aaa 330
 Gln Asp Trp Pro Glu Gly Leu Leu Gln Glu Xaa Glu Lys
 10 15 20

 gta ctc tgc gat gct ggt ttt tta ggt gat gcc tta caa 369
 Val Leu Cys Asp Ala Gly Phe Leu Gly Asp Ala Leu Gln
 25 30

 ctc ttt ctt cag tgc tta gcc ctt gat gaa gat ttt gca 408
 Leu Phe Leu Gln Cys Leu Ala Leu Asp Glu Asp Phe Ala
 35 40 45

 cct gca aag ctg caa gta caa aag att tta tgt gat tta 447

Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu
 50 55

tta tta cct gaa aac tta aaa gaa ggc ctg aag gaa tct 486
 Leu Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser
 60 65 70

tcc tgg agt tca tta cca tgt act aaa aac aga cct ttt 525
 Ser Trp Ser Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe
 75 80 85

gat ttt cat tca gtg atg gaa gag tct cag tct ctc aat 564
 Asp Phe His Ser Val Met Glu Glu Ser Gln Ser Leu Asn
 90 95

gaa cct agc cca aag cag agt gaa gaa ata cca gag gtc 603
 Glu Pro Ser Pro Lys Gln Ser Glu Glu Ile Pro Glu Val
 100 105 110

act tca gag cct gtc aaa gga agc tta aac cgt gct cag 642
 Thr Ser Glu Pro Val Lys Gly Ser Leu Asn Arg Ala Gln
 115 120

tca gca cag tct ata aat tca aca gaa atg cct gcc aga 681
 Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro Ala Arg
 125 130 135

gag gac tgt tta aaa aaa gtg tcc tca gaa cct gtt ctg 720
 Glu Asp Cys Leu Lys Lys Val Ser Ser Glu Pro Val Leu
 140 145 150

tca gtt caa gaa aaa ggt gtt ctg ctg aaa aga aag ttg 759
 Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu
 155 160

tct ctt tta gaa cag gat gtg att gta aat gaa gat gga 798
 Ser Leu Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly
 165 170 175

aga aat aag ctg aaa aaa caa gga gaa act ccc aat gaa 837
 Arg Asn Lys Leu Lys Lys Gln Gly Glu Thr Pro Asn Glu
 180 185

gtc tgt atg ttt tcc tta gct tat ggt gat att cca gaa 876
 Val Cys Met Phe Ser Leu Ala Tyr Gly Asp Ile Pro Glu
 190 195 200

gaa tta atc gat gtc tca gat ttc gag tgt tct ctc tgc 915
 Glu Leu Ile Asp Val Ser Asp Phe Glu Cys Ser Leu Cys
 205 210 215

atg agg ttg ttt ttt gag cca gta aca acc cct tgc gga 954
 Met Arg Leu Phe Phe Glu Pro Val Thr Thr Pro Cys Gly
 220 225

cat tcg ttc tgt aag aat tgt ctt gag cgt tgt tta gat 993
 His Ser Phe Cys Lys Asn Cys Leu Glu Arg Cys Leu Asp
 230 235 240

cat gca cca tat tgt cct ctt tgc aaa gaa agc tta aat 1032
 His Ala Pro Tyr Cys Pro Leu Cys Lys Glu Ser Leu Asn

245

250

gag tat cta gca gat agg agg tac tgt gtc aca cag ctg 1071
 Glu Tyr Leu Ala Asp Arg Arg Tyr Cys Val Thr Gln Leu
 255 260 265

ttg gaa gaa tta ata gtg aag tat ctg cct gat gaa ctg 1110
 Leu Glu Glu Leu Ile Val Lys Tyr Leu Pro Asp Glu Leu
 270 275 280

tct gag aga aaa aaa ata tat gaa gaa gaa act gct gaa 1149
 Ser Glu Arg Lys Lys Ile Tyr Glu Glu Glu Thr Ala Glu
 285 290

ctc tca cac ttg acc aag aat gtt cca ata ttt gtt tgc 1188
 Leu Ser His Leu Thr Lys Asn Val Pro Ile Phe Val Cys
 295 300 305

act atg gcc tac ccc act gtg cct tgc cct ctc cat gta 1227
 Thr Met Ala Tyr Pro Thr Val Pro Cys Pro Leu His Val
 310 315

ttt gag cca aga tac aga ttg atg att cga aga agt ata 1266
 Phe Glu Pro Arg Tyr Arg Leu Met Ile Arg Arg Ser Ile
 320 325 330

cag act gga acc aaa cag ttt ggc atg tgt gtc agt gat 1305
 Gln Thr Gly Thr Lys Gln Phe Gly Met Cys Val Ser Asp
 335 340 345

aca caa aat agt ttt gca gat tat ggt tgt atg tta caa 1344
 Thr Gln Asn Ser Phe Ala Asp Tyr Gly Cys Met Leu Gln
 350 355

att aga aac gtg cat ttc tta ccg gac gga agg tct gtg 1383
 Ile Arg Asn Val His Phe Leu Pro Asp Gly Arg Ser Val
 360 365 370

gtt gat aca gtt gga gga aag cgg ttt agg gtt tta aaa 1422
 Val Asp Thr Val Gly Gly Lys Arg Phe Arg Val Leu Lys
 375 380

aga gga atg aaa gat gga tat tgc act gcc gac att gaa 1461
 Arg Gly Met Lys Asp Gly Tyr Cys Thr Ala Asp Ile Glu
 385 390 395

tat ctg gaa gat gtt aag gtt gag aat gaa gat gag att 1500
 Tyr Leu Glu Asp Val Lys Val Glu Asn Glu Asp Glu Ile
 400 405 410

aag aat ctc aga gag ctt cat gat ttg gtt tac tct caa 1539
 Lys Asn Leu Arg Glu Leu His Asp Leu Val Tyr Ser Gln
 415 420

gcc tgc agc tgg ttt cag aat tta aga gac aga ttt cga 1578
 Ala Cys Ser Trp Phe Gln Asn Leu Arg Asp Arg Phe Arg
 425 430 435

agc caa att ctt cag cat ttc gga tca atg ccc gag ang 1617
 Ser Gln Ile Leu Gln His Phe Gly Ser Met Pro Glu Xaa
 440 445

gag gaa aac ctt cag gca gcc cct aat gga cct gca tgg 1656
 Glu Glu Asn Leu Gln Ala Ala Pro Asn Gly Pro Ala Trp
 450 455 460

tgt tgg tgg ctt ctt gca gtt ctc cct gta gac cca cga 1695
 Cys Trp Trp Leu Leu Ala Val Leu Pro Val Asp Pro Arg
 465 470 475

tac cag ctg tcg gtt ttg tca atg aag tct ttg aaa gaa 1734
 Tyr Gln Leu Ser Val Leu Ser Met Lys Ser Leu Lys Glu
 480 485

cgg ttg acc aag ata cag cat ata ctg acc tat ttt tct 1773
 Arg Leu Thr Lys Ile Gln His Ile Leu Thr Tyr Phe Ser
 490 495 500

aga gac caa tct aag t a actaactctt tggatctccc 1810
 Arg Asp Gln Ser Lys
 505 506

tttaaagtga ccctaactctg gctgcattga tggccagatt gtctgctgcc 1860
 ttgacacatc tagtgctngg ntttcagaaa tttaatgaaa cttttctttt 1910
 ntccttcgac ctncctgaat catgtggtnt ctgcaaatga atnaccttca 1960
 actaggattt agaccactaa gnaacttgca nncagaaaaan acacgcattg 2010
 aatgtgtgtc gaacctctac attgtgaagt tgcactatgt accatactct 2060
 aaaatgaaat aagaactctt tatgtctgtg agagagtgtg tgtgtgtgtg 2110
 tgcgtgcgtg tgtgcttgtg ggggttgggt agtgtgtgtg tattttctct 2160
 ggcttttaaaa ttttaaaaca aacaaaccaa aaagccatag agagcagaac 2210
 ttgccgaggg tcatttattg cccaagttta caagagtagc gatacaagtt 2260
 tttgcaaatt gaatttgcct cagatatatc tgtcctaattg cttatatttg 2310
 cacaagtatg taaaatatcg tgttgaggat cattctttgt tggaaatact 2360
 gctcttgctg aactgtcttg accattgact atgacacagt ttcttattta 2410
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 ggggcttttc acattaactg cccatttgtg taatttatag tttgacatga 2660
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 tttatgtaag taatttgtaa aagtttctta aaatttttgc ttttgcttat 2960
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 Ala Leu Gln Leu Phe Leu Gln Cys Leu Ala Leu Asp Glu Asp Phe
 35 40 45
 Ala Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu Leu
 50 55 60
 Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser Ser Trp Ser
 65 70 75
 Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe Asp Phe His Ser Val
 80 85 90
 Met Glu Glu Ser Gln Ser Leu Asn Glu Pro Ser Pro Lys Gln Ser
 95 100 105
 Glu Glu Ile Pro Glu Val Thr Ser Glu Pro Val Lys Gly Ser Leu
 110 115 120
 Asn Arg Ala Gln Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro
 125 130 135
 Ala Arg Glu Asp Cys Leu Lys Lys Val Ser Ser Glu Pro Val Leu
 140 145 150
 Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu Ser Leu
 155 160 165
 Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly Arg Asn Lys Leu
 170 175 180
 Lys Lys Gln Gly Glu Thr Pro Asn Glu Val Cys Met Phe Ser Leu
 185 190 195
 Ala Tyr Gly Asp Ile Pro Glu Glu Leu Ile Asp Val Ser Asp Phe

200										205					210				
Glu	Cys	Ser	Leu	Cys	Met	Arg	Leu	Phe		Phe	Glu	Pro	Val	Thr	Thr				
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Pro	Cys	Gly	His	Ser	Phe	Cys	Lys	Asn		Cys	Leu	Glu	Arg	Cys	Leu				
				230										235		240			
Asp	His	Ala	Pro	Tyr	Cys	Pro	Leu	Cys		Lys	Glu	Ser	Leu	Asn	Glu				
				245										250		255			
Tyr	Leu	Ala	Asp	Arg	Arg	Tyr	Cys	Val		Thr	Gln	Leu	Leu	Glu	Glu				
				260										265		270			
Leu	Ile	Val	Lys	Tyr	Leu	Pro	Asp	Glu		Leu	Ser	Glu	Arg	Lys	Lys				
				275										280		285			
Ile	Tyr	Glu	Glu	Glu	Thr	Ala	Glu	Leu		Ser	His	Leu	Thr	Lys	Asn				
				290										295		300			
Val	Pro	Ile	Phe	Val	Cys	Thr	Met	Ala		Tyr	Pro	Thr	Val	Pro	Cys				
				305										310		315			
Pro	Leu	His	Val	Phe	Glu	Pro	Arg	Tyr		Arg	Leu	Met	Ile	Arg	Arg				
				320										325		330			
Ser	Ile	Gln	Thr	Gly	Thr	Lys	Gln	Phe		Gly	Met	Cys	Val	Ser	Asp				
				335										340		345			
Thr	Gln	Asn	Ser	Phe	Ala	Asp	Tyr	Gly		Cys	Met	Leu	Gln	Ile	Arg				
				350										355		360			
Asn	Val	His	Phe	Leu	Pro	Asp	Gly	Arg		Ser	Val	Val	Asp	Thr	Val				
				365										370		375			
Gly	Gly	Lys	Arg	Phe	Arg	Val	Leu	Lys		Arg	Gly	Met	Lys	Asp	Gly				
				380										385		390			
Tyr	Cys	Thr	Ala	Asp	Ile	Glu	Tyr	Leu		Glu	Asp	Val	Lys	Val	Glu				
				395										400		405			
Asn	Glu	Asp	Glu	Ile	Lys	Asn	Leu	Arg		Glu	Leu	His	Asp	Leu	Val				
				410										415		420			
Tyr	Ser	Gln	Ala	Cys	Ser	Trp	Phe	Gln		Asn	Leu	Arg	Asp	Arg	Phe				
				425										430		435			
Arg	Ser	Gln	Ile	Leu	Gln	His	Phe	Gly		Ser	Met	Pro	Xaa	Arg	Glu				
				440										445		450			
Glu	Asn	Leu	Gln	Ala	Ala	Pro	Asn	Gly		Pro	Ala	Trp	Cys	Trp	Trp				
				455										460		465			
Leu	Leu	Ala	Val	Leu	Pro	Val	Asp	Pro		Arg	Tyr	Gln	Leu	Ser	Val				
				470										475		480			
Leu	Ser	Met	Lys	Ser	Leu	Lys	Glu	Arg		Leu	Thr	Lys	Ile	Gln	His				
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<213> Homo sapiens

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<222> 300
<223> unknown base

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tcagtgtgga gtatctcaaa gcctttcagg ctgtccagaa ttttccaacc 200
aagaagcagc aactacaggg cttttgaacc ctttctttta ctcattcctg 250
atgtttgata cccttggtg aaaacaattc agtaaagcat cctgcctcan 300
accccccccc 310

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<212> DNA
<213> Homo sapiens

<400> 20
gtgcttctt ggttggaaga ttctgg 26

<210> 21
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<400> 21
ccagaatctt ccaaccaaga agcagc 26

<210> 22
<211> 53
<212> DNA
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<400> 22
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tgc 53

<210> 23
<211> 30
<212> DNA
<213> Homo sapiens

<400> 23
ggagctgcca ttagaatcaa gaatctttgc 30

<210> 24

<211> 533
<212> DNA
<213> Homo sapiens

<400> 24
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cagtcacaaa ttgcaacaa ataattacaa aagtttctag ggcagcatga 150
atataaacca tggtgcagca tggatgatcta actgtgatat gaataaggca 200
taactaacat ttgcaccgag accagaatta aaaacaaaaa caaactttaa 250
aagcttagtt ctatattaaa cttcttctct tttcccagat ccttaatggg 300
tttatactat gcattttttt ttaaaacaaa cacatcatgt caaactataa 350
attacacaaa tgggcagtta atgtgaaaag cccctaaaaa tgtacaaact 400
aactggtact gaattgagtt ctccctttac ctttatgtac aattaaatgt 450
aaaccatatt ttcacagttt tgagtgtttt atgaatagat gcacagtacc 500
atgtcagggt tacaattggt cctgaaaact ggc 533

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<211> 433
<212> DNA
<213> Homo sapiens

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ttccgcccag gacaccggt tgtccttggt gaagtcagcc atgagcagga 100
cctggccaac cagcgccggc agggaaggca ggtctcccag gttcgccttg 150
aggaagccga gggcatctc ccggaattcc ttgatggagg tgccccgggt 200
gggcttggtca aacagtacca gctcccgccg ggggcccgcac ccgaccgggc 250
cttgaggtcg agggctctct caatgccaca cttgatgggt acatccttgt 300
cccgccagag cccgctgtac acctgctggc ccggggcaca cgagaagcag 350
gtcctccact ccaccatag cagctcacac aggtcctggc agacggagcc 400
cgagatgatc cccttgcggt actggtcaca aat 433

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<400> 26
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<210> 27
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<212> DNA
<213> Homo sapiens

<400> 27
ctagagacca atctaagtaa 20

<210> 28
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<400> 28
atggtggagt ggaggacctg 20

<210> 29
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<212> DNA
<213> Homo sapiens

<400> 29
ctccaacacc aagtactctt ga 22